

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 27, 2003, 11:04:55 ; Search time 1982 Seconds
(without alignments)
6666.907 Million cell updates/sec

Title: US-09-987-899-5
Perfect score: 323
Sequence: 1 cgactgtgtgaagcaggtgg.....ccgcgcgcgcgcgcgcgcgc 323

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2889711 seqs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sta:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sta:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sv:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	311	96.3	830	8	MZEPCCSSU	D00170 Zea mays mRNA
2	311	96.3	830	8	ZMRUBSSU	X06535 Maize mRNA
3	295	91.3	1648	8	ZMRBBS	Y03122 Maize rbcS
4	271	83.9	1274	8	ZMRUBSMU	Y09114 Z.mays rubi
5	222.6	68.9	2328	8	SCFECSLA	M86717 Saccharum h
6	201.8	62.5	808	8	RICCPBCLA	L22155 Oryza sativ
7	201.8	62.5	830	8	RICRUBPCA	D00643 Oryza sativ
8	201.8	62.5	14590	8	CNS08C70	AL71739 Oryza sat
9	198.8	61.5	960	6	E06908	E06908 Zoyzia rbes
10	198.6	61.5	854	8	AF017364	AF017364 Oryza sat
11	197	61.0	835	8	AF052305	AF052305 Oryza sat
12	192.2	59.5	591	8	AB020942	AB020942 Secale ce
13	192.2	59.5	604	8	AB020944	AB020944 Agropyron
14	192.2	59.5	787	8	AB020954	AB020954 Triticum
15	192.2	59.5	895	8	RICRUBPC2	D00644 Oryza sativ
16	190.6	59.0	638	8	AB042065	AB042065 Triticum
17	190.6	59.0	781	8	AB020953	AB020953 Aegilops
18	190.6	59.0	787	8	AB020955	AB020955 Triticum
19	190.6	59.0	12767	2	CNS0984U	EX119951 Oryza sat
20	189.6	58.7	845	8	SCR131737	AT11737 Secale ce
21	189	58.5	504	8	AF192776	AF192776 Avena cla
22	189	58.5	504	8	AF192779	AF192779 Avena mar
23	189	58.5	605	8	AB020943	AB020943 Hordeum v
24	189	58.5	611	8	AB020937	AB020937 Aegilops
25	189	58.5	781	8	AB020958	AB020958 Triticum
26	189	58.5	2205	8	WHTRUBIAA	M37328 T.aestivum
27	189	58.5	5980	8	AB042069	AB042069 Triticum
28	188	58.2	789	8	AB020959	AB020959 Secale ce
29	187.4	58.0	600	8	AF202645	AF202645 Avena cla
30	187.4	58.0	604	8	AB020939	AB020939 Triticum
31	187.4	58.0	607	8	AB020938	AB020938 Aegilops
32	187.4	58.0	611	8	TARUB1	X00234 Wheat mRNA
33	187.4	58.0	728	8	AB020952	AB020952 Aegilops
34	187.4	58.0	792	8	AB020949	AB020949 Aegilops
35	187.4	58.0	792	8	AB020950	AB020950 Aegilops
36	187.4	58.0	985	8	AB042068	AB042068 Triticum
37	185.8	57.5	504	8	AF192773	AF192773 Avena aga
38	185.8	57.5	605	8	AB020932	AB020932 Aegilops
39	185.8	57.5	605	8	AB020933	AB020933 Aegilops
40	185.8	57.5	605	8	AB020934	AB020934 Aegilops
41	185.8	57.5	605	8	AB020935	AB020935 Aegilops
42	185.8	57.5	605	8	AB020936	AB020936 Aegilops
43	185.8	57.5	620	8	AF202648	AF202648 Avena mar
44	185.8	57.5	787	8	AB020946	AB020946 Aegilops
45	185.8	57.5	875	8	SCR131738	AJ131738 Secale ce

ALIGNMENTS

RESULT 1
MZEPCCSSU
LOCUS
DEFINITION Zea mays mRNA for ribulose 1,5-bisphosphate carboxylase small subunit, complete cds.
830 bp mRNA linear PLN 13-NOV-1997
ACCESSION D00170
VERSION D00170.1 GI:217963
KEYWORDS RuBPC; ribulose-1,5-bisphosphate carboxylase; small subunit.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 830)
AUTHORS Matsuoaka,M., Kano-Murakami,Y., Tanaka,Y., Ozeki,Y. and Yamamoto,N.

REFERENCE	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD									
AUTHORS	Clade; Panicoidae; Andropogoneae; Zea.									
TITLE	1 (bases 1 to 1648)									
	Lebrun, M., Waksman, G. and Freyssonnet, G.									
	Nucleotide sequence of a gene encoding corn									
	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit									
	(rbcs)									
JOURNAL	Nucleic Acids Res. 15 (10), 4360 (1987)									
MEDLINE	87231019									
PUBMED	3588298									
REFERENCE	2 (bases 1 to 1648)									
AUTHORS	Freyssonnet, G.									
TITLE	Direct Submission									
JOURNAL	Submitted (16-Oct-1987)									
FEATURES	Location/Qualifiers									
source	1..1648									
	/organism="Zea mays"									
	/mol_type="genomic DNA"									
	/strain="F2"									
	/db_xref="taxon:4577"									
CAAT_signal	359..362									
TATA_signal	398..403									
gene	join(491..637,801..1163)									
	/gene="rbcs"									
CDS	join(491..637,801..1163)									
	/gene="rbcs"									
	/EC number="4.1.1.39"									
	/codon_start=1									
	/product="ribulose 1,5-bisphosphate carboxylase/oxygenase"									
	/protein_id="CA68419.1"									
	/db_xref="GI:22465"									
	/db_xref="SWISS-PROT:P05348"									
	/translation="MAPTVMMASATVAPFQGLKSTASLPVARRSRSLGNTVNSGGR									
	IRCWQMPAYGNKKFETLSYLPSTDDLKQVDYLNRNGWIPCLFESKVGFEVYRENS									
	SPCYDGRYWTWKLPWFMGCDNATQVYKEIQEAIKSPYDAFHRVIGFDNIIKQTCQCVSF									
	IAYKPGSD"									
exon	491..637									
	/gene="rbcs"									
	/number=1									
misc_feature	631..632									
	/gene="rbcs"									
intron	/note="pot. site of cleavage of transit peptide"									
	638..800									
	/gene="rbcs"									
	/number=1									
exon	801..1160									
	/gene="rbcs"									
	/number=2									
BASE COUNT	368 a 509 c 411 g 360 t									
ORIGIN										
Query Match	91.3%; Score 295; DB 8; Length 1648;									
Best Local Similarity	98.8%; Pred.No. 2.1e-45;									
Matches 319; Conservative	0; Mismatches 0; Indels 4; Gaps 2;									
QY	1 CGACCTGCTGAAGCAGGTGGACTACCTGCTGCGCAACGGCTGGATACCTCCCTCCAGATT 60									
Db	CGACCTGCTGAAGCAGGTGGACTAC---CTGCGCAACGGCTGGATACCTCCCTCCAGATT 922									
QY	61 CAGCAGGTCCGCTTCGTGTACCGCGAGAACTCCACTCCCTCCGTGCTACTACGACGGCCG 120									
Db	923 CAGCAAGGTCCGCTTCGTGTACCGCGAGAACTCCACTCCCTCCGTGCTACTACGACGGCCG 982									
QY	121 CTACTGCACCATGTGGAAGCATGCCCATGTTCCGGCTGCAACGACGCCACCCAGGTGTACA 180									
Db	983 CTACTGCACCATGTGGAAGC--TGCCCATGTTCCGGCTGCAACGACGCCACCCAGGTGTACA 1041									
QY	181 AGCAGGTGCAAGGAGGCCATCAAAATCTCTACCCGACGGCTTCCACCGGCTCATCGGCTTCG 240									
Db	1042 AGCAGTGCAGGAGGCCATCAAAATCTCTACCCGACGGCTTCCACCGGCTCATCGGCTTCG 1101									
QY	241 ACAACATCAAGCAGACGCAGTGGCTCAGCTTCATCGCTTACATCGCTTACAAGCCGCCGCGAGCACT 300									

BASE COUNT		40123 a 31871 c 33174 g 40721 t		1 others	
ORIGIN		/clone_lib="OSUNBa"			
Query Match		62.5%; Score 201.8; DB 8; Length 145890;			
Best Local Similarity		81.0%; Pred. No. 3.3e-28;			
Matches		247; Conservative 0; Mismatches 57; Indels 1; Gaps 1;			
QY	2	GACCTGCTGAAGCAGGTGGAGTACCTGCTGCGCAACGGTGGATACCCCTGCTCGAGTTC	61		
Db	82537	GACCTCTGAAGCAGATCGAGTACCTGCTCGTTCGATGCGGAGGAGTTC	82596		
QY	62	AGCAAGGTTCGGTTCGTTACCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCCGC	121		
Db	82597	AGCAAGGTTCGGATTCGTTACCGTGAGAACACAGATCCCCCGGATACGATGGCAGG	82656		
QY	122	TACTGGACCATGTGGAAGCATGCCCATGTTCGGGTGCACGACGCCACCCAGGTGTACAA	181		
Db	82657	TACTGGACCATGTGGAAGC-TGCCCATGTTCGGGTGCACTGACGCCACCCAGGTGTCAA	82715		
QY	182	GGAGCTGAGGAGGCCATCAATCTTACCGGAGCCCTTCCACCGCTCATCGGCTTCGA	241		
Db	82716	GGAGCTGAGGAGGCCAAGAGGCGTACCCGTGATCATCGTTCGTTATCATCGGCTTCGA	82775		
QY	242	CAACATCAAGCAGAGCGAGTGGTTCAGCTTCATCGCTTACAGCCCGGGCAGCGCACTA	301		
Db	82776	CAACGTCAAGCAGGTGCACTCATCAGCTTCATCGCTTACAGCCCGGGCTGCGAGGA	82835		
QY	302	GACCGGCC	311		
Db	82836	GTCTG	82840		
RESULT 9					
E06908					
LOCUS					
DEFINITION					
Zoyzia rhes gene.					
ACCESSION					
E06908.1 GI:2175064					
VERSION					
JP 1994070781-A/1.					
KEYWORDS					
unidentified					
SOURCE					
unclassified.					
REFERENCE					
1 (bases 1 to 960)					
AUTHORS					
Uchida, E.					
TITLE					
INDUCTION OF GENE MANIFESTATION					
JOURNAL					
Patent: JP 1994070781-A 1 15-MAR-1994;					
COMMENT					
JAPAN TAAFU GLASS:KK					
OS Zoyzia					
PN JP 1994070781-A/1					
PD 15-MAR-1994					
PF 20-JUN-1991 JP 1991174806					
PI UCHIDA ETSUKO					
PC C12N15/82,A01H1/00//C12N5/10,(C12N5/10,C12R1:91); CC					
strandedness: Double;					
CC topology: Linear;					
FH Key Location/Qualifiers					
FH TATA_signal 88..94					
FT CDS 341..829					
FT 1,5-diphosphate					
FT /product="small subunit of ribulose FT					
FT carboxylase oxidase'					
FT /gene="rbcS".					
FT Location/Qualifiers					
FT 1..960					
/organism="unidentified"					
/mol_type="genomic DNA"					
/db_xref="taxon:32644"					
BASE COUNT					
201 a 285 c 273 g 201 t					
ORIGIN					
Query Match					
61.5%; Score 198.8; DB 6; Length 960;					
BASE COUNT					
201 a 285 c 273 g 201 t					
ORIGIN					

Best Local Similarity		79.7%; Pred. No. 1.9e-27;	
Matches		247; Conservative 0; Mismatches 62; Indels 1; Gaps 1;	
QY	2	GACCTGCTGAAGCAGGTGGAGTACCTGCTGCGCAACGGTGGATACCCCTGCTCGAGTTC	61
Db	532	GACCTCTCAAGCAGATCGAGTACCTAATCCGCTCAACTGGATCCCGTGCCTCGAGTTC	591
QY	62	AGCAAGGTTCGGTTCGTTACCGGAGAACTCCACCTCCCGTGTCTACTACGACGGCCGC	121
Db	592	AGCAAGGTTCGGCTTCGTTCCGGGAGAACGCCAGTCTCCCGGGTACTACGACGGCCGC	651
QY	122	TACTGGACCATGTGGAAGCATGCCCATGTTCGGGTGCACGACGCCACCCAGGTGTACAA	181
Db	652	TACTGGACCATGTGGAAGC-TCCCATGTTCGGGTGCACCGACGCCACCTACAGTGTCTCA	710
QY	182	GGAGCTGAGGAGGCCATCAATCTTACCGGAGCCCTTCCACCGGCTCATCGGCTTCGA	241
Db	711	GGAGATGGAGGAGTCAAGGGGGCTTACCCGACTGCTTCATCCGCTCATCGGCTTCGA	770
QY	242	CAAATCAAGCAGAGCGAGTGGTTCAGCTTCATCGCTTACAGCCCGGGCAGCGACTA	301
Db	771	CAATCTCAGGAGGTGCGATGATCAGTTTCATCGCTTACAGCCAGAGGGCGCAACTA	830
QY	302	GACCGGCC	311
Db	831	AGCGCAGCTC	840
RESULT 10			
AF017364			
LOCUS			
DEFINITION			
Oryza sativa ribulose 1,5-bisphosphate carboxylase small subunit mRNA, complete cds.			
ACCESSION			
AF017364			
VERSION			
AF017364.1 GI:2407282			
KEYWORDS			
Oryza sativa (indica cultivar-group)			
SOURCE			
Oryza sativa (indica cultivar-group)			
ORGANISM			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.			
REFERENCE			
1 (bases 1 to 854)			
AUTHORS			
Lee M.C., Kim, C.S. and Eun, M.Y.			
TITLE			
Characterization of Ribulose 1,5-bisphosphate carboxylase small subunit from rice			
JOURNAL			
Unpublished			
REFERENCE			
2 (bases 1 to 854)			
AUTHORS			
Lee, M.C., Kim, C.S. and Eun, M.Y.			
TITLE			
Direct Submission			
JOURNAL			
Submitted (07-AUG-1997) CytoGenetics, International Institute of Agricultural Science and Technology, Sedun-Dong, RDA, Suwon 441-707, Korea			
FEATURES			
Location/Qualifiers			
source			
1..854			
/organism="Oryza sativa (indica cultivar-group)"			
/mol_type="mRNA"			
/strain="Milkyang 23"			
/db_xref="taxon:39946"			
/clone="KCDM2416"			
/dev_stage="immature seed (milky stage)"			
83..610			
/codon_start=1			
/product="ribulose 1,5-bisphosphate carboxylase small subunit"			
/protein_id="BAB70544.1"			
/db_xref="GI:2407283"			
/translation="MAPSVMASSATTVPQGLKSTAGMPVARRSGNSFGVNSNGR IRCMQWPIEGIKKFTLLKQIEYLLRSKWVPCLSFSKVGFFVIRENH RSPGYDGRYWTWKLPMFGCTDATQVLKELEAKKAYPDFAFRIITFDNVRQVLIS FIAYKPPGCEESGNN"			
CDS			
173 a 239 c 230 g 212 t			
BASE COUNT			
173 a 239 c 230 g 212 t			
ORIGIN			
Query Match			
61.5%; Score 198.8; DB 6; Length 960;			
BASE COUNT			
201 a 285 c 273 g 201 t			
ORIGIN			

```
Query Match      61.5%; Score 198.6; DB 8; Length 854;
Best Local Similarity 80.3%; Pred. No. 2e-27;
Matches 245; Conservative 0; Mismatches 59; Indels 1; Gaps 1;

QY 2 GACCTGCTGAAGCAGGTGGACTACCTGCTGCGCAACGGCTGGATACCCCTCGAGTTC 61
   |||||
Db 296 GACCTCTGAAGCAGATCGAGTACCTCCCTCGTTCGAAGTGGGTGCCCTCGAGTTC 355
   |||||
QY 62 AGCAAGGTGGCTTCGTGTACCGCGAGAACTCCACCTCCCGCTGCTACTACGACGGCCGC 121
   |||||
Db 356 AGCAAGGTGGATTTGCTACCTGTGAGAACACAGATCCCCCGGATACGATGGCAGG 415
   |||||
QY 122 TACTGACCATGTGGAAGCATGCCATGTCACCGGAGAACTCCACCTCCCGCTGCTACTACGACGGCCGC 121
   |||||
Db 416 TACTGACCATGTGGAAGC-TGCCCATGTTCCGGGTGCACTGACGCCACCCAGGTGCTCAA 474
   |||||
QY 182 GGAGCTGCGAGGAGCCATCAATCCTACCGGAGCGCTTCCACCGGTCTATCGGCTTCCA 241
   |||||
Db 475 GGAGCTGCGAGGAGGCCAAGAGCGGTACCTGTATGATTCGTCCGTATCATCGGCTTCCA 534
   |||||
QY 242 CAACATCAAGCAGACGAGTGGCTCAGCTTCATCGCTCAAGACCCCGGCGACGACTA 301
   |||||
Db 535 CAACGTGAGGAGTGGCTCAGCTTCATCGCTCAAGACCCCGGCGTGGCAGGA 594
   |||||
QY 302 GACCG 306
   |||
Db 595 GTCTG 599

RESULT 11
AF052305      835 bp mRNA linear PLN 18-APR-1998
LOCUS      Oryza sativa ribulose 1,5-bisphosphate carboxylase small subunit
DEFINITION      mRNA, complete cds.
ACCESSION      AF052305
VERSION      AF052305.1 GI:3063523
KEYWORDS
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 835)
AUTHORS      Yoon,U.H., Hahn,J.H., Yun,C.-H. and Eun,M.Y.
TITLE      Molecular cloning and characterization of cDNA encoding the small
            subunit of ribulose 1,5-bisphosphate carboxylase in rice
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 835)
AUTHORS      Yoon,U.H., Hahn,J.H., Yun,C.-H. and Eun,M.Y.
TITLE      Direct Submission
JOURNAL      Submitted (05-MAR-1998) Cytogenetics, National Institute of
            Agricultural Science and Technology, Seodun-dong, Suwon 441-707,
            Korea

FEATURES
    source
        1..835
            /organism="Oryza sativa"
            /mol_type="mRNA"
            /cultivar="lipoombyeo"
            /db_xref="taxon:4530"
            /clone="Y83"
            /cell_type="seedling"
        46..573
            /note="RRBC83"
            /codon_start=1
            /product="ribulose 1,5-bisphosphate carboxylase small
            subunit"
            /protein_id="AAC14064.1"
            /db_xref="GI:3063524"
            /translation="WAPSVMASATTAPFQGLKSTAGMPVARRSGNSFGVNSNGGR
            IRCMQVPIEGIKKFTLSJLPLTVEDLLKQIELLRSKWYPCLEFVKGVFVRENH
            RSPGYDGRYWTWMLPWFPGCTDATQVLKELEAKKANPDFAFRIIGFNVQVQLIS
            FIAYKPPGCEESGNN"

BASE COUNT      187 a 226 c 221 g 201 t

Query Match      61.0%; Score 197; DB 8; Length 835;
Best Local Similarity 80.0%; Pred. No. 4.1e-27;
Matches 244; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

QY 2 GACCTGCTGAAGCAGGTGGACTACCTGCTGCGCAACGGCTGGATACCCCTCGAGTTC 61
   |||||
Db 259 GACCTCTGAAGCAGATCGAGTACCTCCCTCGTTCGAAGTGGGTGCCCTCGAGTTC 318
   |||||
QY 62 AGCAAGGTGGCTTCGTGTACCGCGAGAACTCCACCTCCCGCTGCTACTACGACGGCCGC 121
   |||||
Db 319 AGCAAGGTGGATTCGTTCTACCGTGAGAACCAAGATCCCGCGATATTACGATGGCAGG 378
   |||||
QY 122 TACTGACCATGTGGAAGCATGCCATGTCACCGGAGAACTCCACCTCCCGCTGCTACTACGACGGCCGC 181
   |||||
Db 379 TACTGACCATGTGGAAGC-TGCCCATGTTCCGGGTGCACTGACGCCACCCAGGTGCTCAA 437
   |||||
QY 182 GGAGCTGCGAGGAGCCATCAATCCTACCGGAGCGCTTCCACCGGTCTATCGGCTTCCA 241
   |||||
Db 438 GGAGCTGCGAGGAGGCCAAGAGCGGTACCTGTATGATTCGTCCGTATCATCGGCTTCCA 497
   |||||
QY 242 CAACATCAAGCAGACGAGTGGCTCAGCTTCATCGCTCAAGACCCCGGCGACGACTA 301
   |||||
Db 498 CAACGTGAGGAGTGGCTCAGCTTCATCGCTCAAGACCCCGGCGTGGCAGGA 557
   |||||
QY 302 GACCG 306
   |||
Db 558 GTCTG 562

RESULT 12
AB020942      591 bp DNA linear PLN 27-JAN-2001
LOCUS      Secale cereale DNA for ribulose-1,5-bisphosphate
DEFINITION      carboxylase/oxygenase small subunit, partial cds, clone Sec-A.
ACCESSION      AB020942
VERSION      AB020942.1 GI:4038688
KEYWORDS      Small subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase.
SOURCE      Secale cereale (rye)
ORGANISM      Secale cereale
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Secale.
REFERENCE      1 (sites)
AUTHORS      Sasanuma,T. and Miyashita,N.T.
TITLE      Subfamily divergence in the multigene family of
            ribulose-1,5-bisphosphate carboxylase/oxygenase (rbcS) in Triticeae
            and its relatives
JOURNAL      Genes Genet. Syst. 73 (5), 297-309 (1998)
MEDLINE      99185472
PUBMED      10085553
REFERENCE      2 (bases 1 to 591)
AUTHORS      Sasanuma,T.
TITLE      Direct Submission
JOURNAL      Submitted (09-DEC-1998) Tsuneeo Sasanuma, Kyoto University,
            Laboratory of Plant Genetics, Graduate School of Agriculture;
            Sakyo-ku, Kitashirakawa Oiwakecho, Kyoto, Kyoto 606-8502, Japan
            (E-mail:sasanuma@kais.kyoto-u.ac.jp, Tel:81-75-753-6145(ex.6145),
            Fax:81-75-753-6146)

FEATURES
    Location/Qualifiers
        1..591
            /organism="Secale cereale"
            /mol_type="genomic DNA"
            /cultivar="Prolific"
            /db_xref="taxon:4550"
            /clone="Sec-A"
            join(1..133,227..591)
            /gene="rbcS"
            join(<1..133,227..591)
            /gene="rbcS"
            /codon_start=2
            /product="ribulose-1,5-bisphosphate carboxylase/oxygenase"
    gene
    CDS
```


This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 27, 2003, 10:58:50 ; Search time 216 Seconds
(without alignments)
4036.660 Million cell updates/sec

Title: US-09-987-899-5
Perfect score: 323
Sequence: 1 cgactctgtgaacgaggtgg.....ccgcgcgcgcgcgcgcgcgc 323

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 19Jun03.*
1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198.8	61.5	960	15	AAQ62173 rbcS subunit of ri
2	177	54.8	1110	24	ABK86728 Rice rubisco synth
3	125.6	38.9	471	24	ABL93405 Arabidopsis thalia
4	125.6	38.9	546	21	AAC48433 Arabidopsis thalia
5	125.6	38.9	572	21	AAC42417 Arabidopsis thalia
6	125.6	38.9	599	21	AAC47674 Arabidopsis thalia
7	125.6	38.9	681	24	ABQ65767 Arabidopsis thalia
8	125.6	38.9	724	24	ABL49453 Sequence #55 used

9	125.6	38.9	724	24	ABK30640 Plant dwarfing/stu
10	125.6	38.9	726	24	ABK30788 Plant dwarfing/stu
11	125.6	38.9	771	24	ABN99150 Arabidopsis thalia
12	125.6	38.9	785	24	ABN99094 Arabidopsis thalia
13	125.6	38.9	1164	21	AAC52133 Arabidopsis thalia
14	125.6	38.9	1205	24	ABN98273 Arabidopsis thalia
15	124	38.4	672	24	ABQ65829 Arabidopsis thalia
16	124	38.4	711	24	ABL49430 Arabidopsis thalia
17	124	38.4	711	24	ABK30617 Plant dwarfing/stu
18	124	38.4	739	24	ABK30768 Plant dwarfing/stu
19	123.2	38.1	570	21	AAA32041 Plant microsatelli
20	121.4	37.6	546	21	AAC48432 Arabidopsis thalia
21	121.4	37.6	632	24	ABQ66100 Arabidopsis thalia
22	121.4	37.6	767	24	ABN99163 Arabidopsis thalia
23	121.4	37.6	780	24	ABN99112 Arabidopsis thalia
24	121.4	37.6	1135	21	AAC51817 Arabidopsis thalia
25	117	36.2	606	21	AAA32043 Plant microsatelli
26	116.4	36.0	934	25	ABQ83412 Coffee rbcS protei
27	110.6	34.2	578	25	ABX56841 Arabidopsis thalia
28	107.8	33.4	2034	25	ABQ83211 Coffee rbcS gene S
29	107.2	33.2	453	24	ABL93846 Arabidopsis thalia
30	95.6	29.6	273	25	ABX30796 Human GDP-mannose
31	93	28.8	469	24	ABR92079 Arabidopsis RUBISC
32	92.2	28.5	502	21	AAA31309 Plant microsatelli
33	90.2	27.9	499	24	AAD35635 Nicotiana benthami
34	85.6	26.5	484	21	AAA31305 Plant microsatelli
35	84	26.0	479	21	AAA31292 Plant microsatelli
36	83	25.7	481	21	AAA31306 Plant microsatelli
37	79	24.5	479	21	AAA32042 Plant microsatelli
38	74.4	23.0	375	21	AAC45166 Arabidopsis thalia
39	74.2	23.0	477	21	AAC37237 Arabidopsis thalia
40	74	22.9	450	21	AAA31250 Plant microsatelli
41	66.2	20.5	457	21	AAA31269 Plant microsatelli
42	65.2	20.2	433	21	AAA31284 Plant microsatelli
43	64.6	20.0	479	21	AAA31291 Plant microsatelli
44	60.6	18.8	336	16	AAQ87824 Agmenellum quadrup
45	60.6	18.8	4234	16	AAQ87819 Agmenellum quadrup

ALIGNMENTS

RESULT 1
AAQ62173
ID AAQ62173 standard; cDNA; 960 BP.
XX AAQ62173;
AC AAQ62173;
XX
DT 16-NOV-1994 (first entry)
XX
DE rbcS subunit of ribulose-1,5-diphosphate carboxylase/oxidase.
XX
KW Ribulose-1,5-diphosphate carboxylase/oxidase; enzyme; rbcS;
KW subunit; gene expression; induction; irradiation; light;
KW promoter; plant; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_signal /tag= a
FT /note= "transcription start"
FT misc_signal /tag= b
FT /note= "translation initiation codon"
FT misc_signal /tag= c
FT /note= "translation initiation codon"
FT misc_signal /tag= d
FT /note= "stop codon"
XX JP06070781-A.

PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0133456.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134378.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139859.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142330.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.

PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 21-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157173.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.

PR	06-JUL-1999;	99US-0142390.
PR	08-JUL-1999;	99US-0142803.
PR	09-JUL-1999;	99US-0142920.
PR	12-JUL-1999;	99US-0142977.
PR	13-JUL-1999;	99US-0143542.
PR	14-JUL-1999;	99US-0143624.
PR	15-JUL-1999;	99US-0144005.
PR	16-JUL-1999;	99US-0144085.
PR	16-JUL-1999;	99US-0144086.
PR	19-JUL-1999;	99US-0144325.
PR	19-JUL-1999;	99US-0144331.
PR	19-JUL-1999;	99US-0144332.
PR	19-JUL-1999;	99US-0144333.
PR	19-JUL-1999;	99US-0144334.
PR	19-JUL-1999;	99US-0144335.
PR	20-JUL-1999;	99US-0144352.
PR	20-JUL-1999;	99US-0144632.
PR	20-JUL-1999;	99US-0144684.
PR	21-JUL-1999;	99US-0144814.
PR	21-JUL-1999;	99US-0145086.
PR	21-JUL-1999;	99US-0145088.
PR	22-JUL-1999;	99US-0145085.
PR	22-JUL-1999;	99US-0145087.
PR	22-JUL-1999;	99US-0145089.
PR	22-JUL-1999;	99US-0145192.
PR	23-JUL-1999;	99US-0145145.
PR	23-JUL-1999;	99US-0145218.
PR	23-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145276.
PR	27-JUL-1999;	99US-0145313.
PR	27-JUL-1999;	99US-0145318.
PR	27-JUL-1999;	99US-0145319.
PR	28-JUL-1999;	99US-0145951.
PR	02-AUG-1999;	99US-0146386.
PR	02-AUG-1999;	99US-0146388.
PR	02-AUG-1999;	99US-0146389.
PR	03-AUG-1999;	99US-0147038.
PR	04-AUG-1999;	99US-0147204.
PR	04-AUG-1999;	99US-0147302.
PR	05-AUG-1999;	99US-0147192.
PR	05-AUG-1999;	99US-0147260.
PR	06-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147416.
PR	09-AUG-1999;	99US-0147493.
PR	09-AUG-1999;	99US-0147935.
PR	10-AUG-1999;	99US-0148171.
PR	11-AUG-1999;	99US-0148319.
PR	12-AUG-1999;	99US-0148341.
PR	13-AUG-1999;	99US-0148565.
PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158212.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	14-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.
Query Match 38.9%; Score 125.6; DB 21; Length 572;		
Best Local Similarity 68.6%; Pred. No. 2.5e-18;		
Matches 203; Conservative 0; Mismatches 89; Indels 4; Gaps 2;		
QY	1	CGACCTGCTGAAGCAGGTGGACTACCTGCTGCGCAACGGCTGGATACCTGCTGCTCGCTCGAGTT 60
Db	266	CGAATTGGCTAAGGAAGTTGACTTATCCGCAACGAAGTGGATTCTTGTGTGAAAT 325
QY	61	C---AGCAAGTCGGCTTCGTGTACGGCGAGACTCCACCTCCCGTGTCTACTACGACGG 117
Db	326	CGAGTTGGAGCACGGATTGTGTACCGTGAGCAGCGTAACCTACCCGGATCTATGATGG 385
QY	118	CGGCTACTGGACCATGTGTGAAGCATGCCCATGTTGGGCTGCAACGACGCCACCCAGGTGT 177
Db	386	ACGGTACTGGACAAATGTGGAGC-TTCCCTTGTTCGGTTGCAACCGACTCCGCTCAAGTGT 444
QY	178	ACAAGAGCTGCAGGAGGCCATCAATCTACCCGAGCGCTTTCACCGGGTCATCGGCT 237
Db	445	TGAGGAAGTGGAGAGTGAAGAGGAGTACCCCAATGCCTTCATTAGGATCATCGGAT 504
QY	238	TCGACAACTCAAGCAGACGCGTGGCTCAGCTTCATCGCTACAAGCCCCCGGC 293
Db	505	TCGACAAACCCCGTCAAGTCCAGTGATCAGTTTCATTGCTTACAAGCCACCAAGC 560
RESULT 6		
AAC47674		
ID	AAC47674 standard; DNA; 599 BP.	
XX	AAC47674;	
AC	AAC47674;	
XX	18-OCT-2000 (first entry)	
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 54694.	

XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX .

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 16-APR-1999; 99US-0128714.

XX 19-APR-1999; 99US-0129845.

XX 21-APR-1999; 99US-0130077.

XX 23-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131449.

XX 30-APR-1999; 99US-0132048.

XX 04-MAY-1999; 99US-0132407.

XX 05-MAY-1999; 99US-0132484.

XX 06-MAY-1999; 99US-0132485.

XX 07-MAY-1999; 99US-0132487.

XX 11-MAY-1999; 99US-0132863.

XX 14-MAY-1999; 99US-0134256.

XX 14-MAY-1999; 99US-0134218.

XX 14-MAY-1999; 99US-0134219.

XX 14-MAY-1999; 99US-0134221.

XX 18-MAY-1999; 99US-0134370.

XX 19-MAY-1999; 99US-0134768.

XX 20-MAY-1999; 99US-0134941.

XX 21-MAY-1999; 99US-0135124.

XX 24-MAY-1999; 99US-0135353.

XX 25-MAY-1999; 99US-0135629.

XX 27-MAY-1999; 99US-0136021.

XX 28-MAY-1999; 99US-0136392.

XX 01-JUN-1999; 99US-0136782.

XX 03-JUN-1999; 99US-0137222.

XX 04-JUN-1999; 99US-0137502.

XX 07-JUN-1999; 99US-0137724.

XX 08-JUN-1999; 99US-0138094.

XX 10-JUN-1999; 99US-0138540.

XX 14-JUN-1999; 99US-0138847.

XX 16-JUN-1999; 99US-0139119.

XX 17-JUN-1999; 99US-0139452.

XX 18-JUN-1999; 99US-0139492.

XX 18-JUN-1999; 99US-0139454.

XX 18-JUN-1999; 99US-0139455.

XX 18-JUN-1999; 99US-0139456.

XX 18-JUN-1999; 99US-0139457.

XX 18-JUN-1999; 99US-0139458.

XX 18-JUN-1999; 99US-0139459.

XX 18-JUN-1999; 99US-0139460.

XX 18-JUN-1999; 99US-0139461.

XX 18-JUN-1999; 99US-0139462.

XX 18-JUN-1999; 99US-0139463.

XX 18-JUN-1999; 99US-0139750.

XX 18-JUN-1999; 99US-0139763.

XX 21-JUN-1999; 99US-0139817.

XX 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.

589 CCGA 592

RESULT 7
 ABQ65767/c
 IID ABQ65767 standard; DNA; 681 BP.
 XX
 XX AC ABQ65767;
 DT 21-AUG-2002 (first entry)
 XX
 XX DE Arabidopsis thaliana polynucleotide SEQ ID NO 344.
 XX
 XX Arabidopsis thaliana; thale cress; plant; transgenic; GMO; disease;
 KW stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide;
 KW insecticide; antibiotic; ds.
 XX
 XX OS Arabidopsis thaliana.
 XX
 XX US2002059663-A1.
 PN
 PD 16-MAY-2002.
 XX
 XX 26-JAN-2001; 2001US-0770149.
 XX
 XX 27-JAN-2000; 2000US-178506P.
 XX
 XX (GORL/) GORLACH J.
 PA (ANY/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUY/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHAW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KRIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 XX
 XX Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
 PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
 PI Hurban P;
 XX
 XX WPI; 2002-479224/51.
 DR
 XX New nucleic acid that hybridizes to Arabidopsis thaliana sequences,
 XX useful e.g. for preparing transgenic plants with increased resistance
 XX or altered metabolism -
 XX
 XX Claim 1; SEQ ID NO 344; 40pp + Sequence Listing; English.
 XX
 XX The invention relates to nucleic acids (I) that hybridise under string-
 XX conditions to any of 999 sequences (ABQ65424-ABQ66422) or their
 XX fragments. (I) are used to express the corresponding polypeptides (II)
 XX to produce genetically modified plant cells or transgenic plants, whi-
 XX ch may have improved resistance to disease or stress, or altered
 XX metabolic/biosynthetic pathways (for production of commercial,
 XX nutritional or medicinal products), or generally any trait of interest
 XX or can be used to screen for biologically active agents (e.g. fungici-
 XX des, insecticides and antibiotics).
 XX Note: The sequence data for this patent did not form part of the prin-
 XX cipal specification, but was obtained in electronic format directly from the
 XX USPTO at seqdata.uspto.gov/sequence.html?DocID=999909770149.

XX	SQ	Sequence 681 BP; 183 A; 143 C; 160 G; 195 T; 0 other;	
		Query Match 38.9%; Score 125.6; DB 24; Length 681;	
		Best Local Similarity 68.6%; Pred. No. 2.5e-18;	
		Matches 203; Conservative 0; Mismatches 89; Indels 4; Gaps 2;	
QY	1	CGACCTGCTGAAGCAGGTGGAGTACCTGCTGCGCAACGGCTGGATACCTGCGCTCGAGTT 60	
DB	472	CGAATTGGCTAAGGAAGTTGACTACCTTCTCCGCAACAATGGATTCTTGTGTTGAATT 413	
QY	61	C---AGCAAGTTCGGCTTCGTGTACCGGAGAACTCCACCTCCCGGTGCTACTACGACGG 117	
DB	412	CGAGTTGGAGCAGCGATTGTGTACCGTGAGCAACGAAACACTCCCGGATACCTACGATGG 353	
QY	118	CCGCTACTGACCAATGTGGAAGCATGCCATGTTTCGGCTGCAACGACGCCACCCAGGTGT 177	
DB	352	ACGCTACTGGACATGTGGAGGC-TTCCATGTTCCGATGCACCGATCCCGCTCAAGTGT 294	
QY	178	ACAAGGAGCTGCGAGGAGGCCATCAAAATCCTACCGGACGCTTCCACCGGTGTCATCGGCT 237	
DB	293	TGAAGGAAGTTGAAGATGCAAGAGGAGTACCGGCGCGCTTCATTAGGATCATCGAT 234	
QY	238	TCGACACATCAAGCAGACGCGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 293	
DB	233	TCGACACACCCGCTCAAGTCCAAATGCATCAGTTTTCATTGCTGCTGCTGCTGCTGCTGCTGCT 178	
XX	RESULT 8		
XX	ABL49453		
ID	ABL49453	standard; cDNA; 724 BP.	
XX	ABL49453;		
XX	01-JUL-2002	(first entry)	
XX	Sequence #55	used to create transgenic plant with dwarf phenotype.	
DE	Transgenic plant;	dwarf phenotype; ss.	
XX	Arabidopsis thaliana.		
XX	WO200208411-A2.		
XX	31-JAN-2002.		
XX	20-JUL-2001;	2001WO-US23315.	
XX	20-JUL-2000;	2000US-219943P.	
XX	(LARG-)	LARGE SCALE BIOLOGY CORP.	
XX	Pogue GP,	Della-Cioppa GR, Wolfe GM, Zheng W;	
XX	WPI;	2002-195875/25.	
XX	Creating transgenic plants	exhibiting a dwarf phenotype useful in	
PT	biopharmaceutical manufacturing,	comprises expressing in the plant a	
PT	gene for dwarfism or stunting	having a sequence selected from 122	
PT	polynucleotide sequences		
XX	Claim 1;	Page 154; 178pp; English.	
XX	This invention relates	to the creation of a transfectant or transgenic	
CC	plant selected from ornamental,	horticultural, forestry, medicinal and	
CC	Nicotiana sp. plants,	all of which exhibit a dwarf phenotype by	
CC	expressing in the plant a DNA	comprising a sequence selected from 122	
CC	polynucleotide sequences.	This sequence represents on of those	
CC	polynucleotide sequences.	The nucleic acid and amino acid sequences are	
CC	useful for producing transgenic	plants exhibiting a dwarf phenotype for	
CC	use in biopharmaceutical	manufacturing. The cDNA sequences may be used	
CC	in recombinant DNA	molecules to direct expression of polypeptides in	
CC	appropriate host cells.		
XX	Reddy SA,	Larrinua MI, Ruegger M, Weglarz T, Blakeslee B;	
XX	Oriedo VBJ,	Savickas JP, McCreary AD, Miller AB, Pogue PG;	
PI	Della-Cioppa RG,	Wolfe MG, Zheng W, Gachotte D, Grosley R, Pell R;	

XX	SQ	Sequence 724 BP; 198 A; 174 C; 156 G; 196 T; 0 other;	
		Query Match 38.9%; Score 125.6; DB 24; Length 724;	
		Best Local Similarity 67.8%; Pred. No. 2.5e-18;	
		Matches 206; Conservative 0; Mismatches 94; Indels 4; Gaps 2;	
QY	1	CGACCTGCTGAAGCAGGTGGAGTACCTGCTGCGCAACGGCTGGATACCTGCGCTCGAGTT 60	
DB	279	CGAATTGGCTAAGGAAGTTGACTACCTTCTCCGCAACAATGGATTCTTGTGTTGAATT 338	
QY	61	C---AGCAAGTTCGGCTTCGTGTACCGGAGAACTCCACCTCCCGGTGCTACTACGACGG 117	
DB	339	CGAGTTAGAGCAGCGATTGTGTACCGTGAGCAACGAAACACTCCCGGATACCTACGATGG 398	
QY	118	CCGCTACTGACCAATGTGGAAGCATGCCATGTTTCGGCTGCAACGACGCCACCCAGGTGT 177	
DB	399	ACGCTACTGGACATGTGGAGGC-TTCCATGTTTCGATGCACCGACTCCGCTCAAGTGT 457	
QY	178	ACAAGGAGCTGCGAGGAGGCCATCAAAATCCTACCGGACGCTTCCACCGGTGTCATCGGCT 237	
DB	458	TGAAGGAAGTTGAAGATGCAAGAGGAGTACCGGCGCGCTTCATTAGGATCATCGAT 517	
QY	238	TCGACACATCAAGCAGACGCGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 297	
DB	518	TCGACACACCCGCTCAAGTCCAAATGCATCAGTTTTCATTGCTGCTGCTGCTGCTGCTGCTGCT 577	
QY	298	ACTA 301	
DB	578	CCGA 581	
XX	RESULT 9		
XX	ABK30640		
ID	ABK30640	standard; cDNA; 724 BP.	
XX	ABK30640;		
XX	23-APR-2002	(first entry)	
XX	Plant dwarfing/stunting	related cDNA seq ID 54.	
DE	Plant;	ss; dwarfism; stunting; EST; expressed sequence tag;	
KW	transgenic plant;	plant metabolism.	
XX	Arabidopsis thaliana.		
XX	WO200208410-A2.		
XX	31-JAN-2002.		
XX	20-JUL-2001;	2001WO-US23120.	
XX	20-JUL-2000;	2000US-219809P.	
XX	20-JUL-2000;	2000US-219810P.	
XX	(DWC)	DOW CHEM CO.	
PA	(REDD/)	REDDY S A.	
PA	(LARR/)	LARRINUA M I.	
PA	(RUEG/)	RUEGGER M.	
PA	(WEG/)	WEGLARZ T.	
PA	(BLAK/)	BLAKESLEE B.	
PA	(ORIE/)	ORIEDO V B J.	
PA	(SAVI/)	SAVICKAS J P.	
PA	(MCCR/)	MCCRERY A D.	
PA	(MILL/)	MILLER A B.	
PA	(GACH/)	GACHOTTE D.	
PA	(GROS/)	GROSLEY R.	
PA	(PELL/)	PELL R.	
XX	Reddy SA,	Larrinua MI, Ruegger M, Weglarz T, Blakeslee B;	
XX	Oriedo VBJ,	Savickas JP, McCreary AD, Miller AB, Pogue PG;	
PI	Della-Cioppa RG,	Wolfe MG, Zheng W, Gachotte D, Grosley R, Pell R;	

[illegible]

PN	EF1033405-A2.	PR	01-JUL-1999;	99US-0142154.
XX		PR	02-JUL-1999;	99US-0142055.
PD	06-SEP-2000.	PR	06-JUL-1999;	99US-0142390.
XX		PR	08-JUL-1999;	99US-0142803.
PF		PR	09-JUL-1999;	99US-0142920.
XX	25-FEB-2000; 2000EP-0301439.	PR	12-JUL-1999;	99US-0142977.
PR		PR	13-JUL-1999;	99US-0143542.
PR	25-FEB-1999;	PR	15-JUL-1999;	99US-0144005.
PR	99US-0121825.	PR	16-JUL-1999;	99US-0144085.
PR	99US-0123180.	PR	16-JUL-1999;	99US-0144086.
PR	05-MAR-1999;	PR	19-JUL-1999;	99US-0144331.
PR	99US-0123548.	PR	19-JUL-1999;	99US-0144332.
PR	23-MAR-1999;	PR	19-JUL-1999;	99US-0144333.
PR	99US-0125788.	PR	19-JUL-1999;	99US-0144334.
PR	99US-0126264.	PR	19-JUL-1999;	99US-0144335.
PR	99US-0126785.	PR	20-JUL-1999;	99US-0144352.
PR	99US-0127462.	PR	20-JUL-1999;	99US-0144632.
PR	99US-0128234.	PR	20-JUL-1999;	99US-0144884.
PR	99US-0128714.	PR	21-JUL-1999;	99US-0144814.
PR	08-APR-1999;	PR	21-JUL-1999;	99US-0145086.
PR	99US-0129845.	PR	21-JUL-1999;	99US-0145088.
PR	99US-0130077.	PR	22-JUL-1999;	99US-0145085.
PR	99US-0130449.	PR	22-JUL-1999;	99US-0145087.
PR	99US-0130510.	PR	22-JUL-1999;	99US-0145089.
PR	99US-0130891.	PR	22-JUL-1999;	99US-0145192.
PR	23-APR-1999;	PR	23-JUL-1999;	99US-0145145.
PR	99US-0131449.	PR	23-JUL-1999;	99US-0145218.
PR	99US-0132048.	PR	23-JUL-1999;	99US-0145224.
PR	99US-0132407.	PR	26-JUL-1999;	99US-0145276.
PR	99US-0132484.	PR	27-JUL-1999;	99US-0145913.
PR	99US-0132485.	PR	27-JUL-1999;	99US-0145918.
PR	06-MAY-1999;	PR	27-JUL-1999;	99US-0145919.
PR	99US-0132486.	PR	28-JUL-1999;	99US-0145951.
PR	06-MAY-1999;	PR	02-AUG-1999;	99US-0146386.
PR	99US-0132487.	PR	02-AUG-1999;	99US-0146388.
PR	99US-0132863.	PR	02-AUG-1999;	99US-0146389.
PR	99US-0134256.	PR	03-AUG-1999;	99US-0147038.
PR	99US-0134218.	PR	04-AUG-1999;	99US-0147204.
PR	99US-0134219.	PR	04-AUG-1999;	99US-0147302.
PR	99US-0134221.	PR	05-AUG-1999;	99US-0147192.
PR	99US-0134370.	PR	05-AUG-1999;	99US-0147260.
PR	99US-0134768.	PR	06-AUG-1999;	99US-0147303.
PR	99US-0134941.	PR	06-AUG-1999;	99US-0147416.
PR	99US-0135124.	PR	09-AUG-1999;	99US-0147493.
PR	99US-0135353.	PR	09-AUG-1999;	99US-0147935.
PR	24-MAY-1999;	PR	10-AUG-1999;	99US-0148171.
PR	99US-0135629.	PR	11-AUG-1999;	99US-0148319.
PR	99US-0136021.	PR	12-AUG-1999;	99US-0148341.
PR	99US-0136392.	PR	13-AUG-1999;	99US-0148565.
PR	99US-0136782.	PR	13-AUG-1999;	99US-0148684.
PR	99US-0137222.	PR	16-AUG-1999;	99US-0149368.
PR	99US-0137528.	PR	17-AUG-1999;	99US-0149175.
PR	99US-0137502.	PR	18-AUG-1999;	99US-0149426.
PR	99US-0137724.	PR	20-AUG-1999;	99US-0149722.
PR	99US-0138094.	PR	20-AUG-1999;	99US-0149723.
PR	99US-0138540.	PR	20-AUG-1999;	99US-0149929.
PR	99US-0138847.	PR	23-AUG-1999;	99US-0149902.
PR	99US-0139119.	PR	23-AUG-1999;	99US-0149930.
PR	99US-0139452.	PR	25-AUG-1999;	99US-0150566.
PR	99US-0139453.	PR	26-AUG-1999;	99US-0150884.
PR	99US-0139492.	PR	27-AUG-1999;	99US-0151065.
PR	99US-0139454.	PR	27-AUG-1999;	99US-0151066.
PR	99US-0139455.	PR	27-AUG-1999;	99US-0151080.
PR	99US-0139456.	PR	30-AUG-1999;	99US-0151303.
PR	99US-0139457.	PR	31-AUG-1999;	99US-0151438.
PR	99US-0139458.	PR	01-SEP-1999;	99US-0151930.
PR	99US-0139459.	PR	07-SEP-1999;	99US-0152363.
PR	99US-0139460.	PR	10-SEP-1999;	99US-0153070.
PR	99US-0139461.	PR	13-SEP-1999;	99US-0153758.
PR	99US-0139462.	PR	15-SEP-1999;	99US-0154018.
PR	99US-0139463.	PR	16-SEP-1999;	99US-0154039.
PR	99US-0139750.			
PR	99US-0139763.			
PR	99US-0139817.			
PR	99US-0139899.			
PR	99US-0140353.			
PR	99US-0140354.			
PR	99US-0140695.			
PR	99US-0140823.			
PR	99US-0140991.			
PR	99US-0141287.			
PR	99US-0141842.			

RESULT 14	
ABN98273	
IID	ABN98273 standard; DNA; 1205 BP.
XX	
AC	
AC	ABN98273;
XX	
DT	01-AUG-2002 (first entry)

this Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 27, 2003, 17:13:01 ; Search time 1942 Seconds
(without alignments)
4042.403 Million cell updates/sec

Title: US-09-987-899-5
Perfect score: 323
Sequence: 1 cgacctgtgaagcaggtgg.....ccgcgccgcgcgcgcgc 323

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:

- 1: em_estba:**
- 2: em_esthum:**
- 3: em_estin:**
- 4: em_estmu:**
- 5: em_estov:**
- 6: em_estpl:**
- 7: em_estro:**
- 8: em_htc:**
- 9: gb_est1:**
- 10: gb_est2:**
- 11: gb_htc:**
- 12: gb_est3:**
- 13: gb_est4:**
- 14: gb_est5:**
- 15: em_estfun:**
- 16: em_estom:**
- 17: em_gss_hum:**
- 18: em_gss_inv:**
- 19: em_gss_pln:**
- 20: em_gss_vrt:**
- 21: em_gss_fun:**
- 22: em_gss_nam:**
- 23: em_gss_mus:**
- 24: em_gss_pro:**
- 25: em_gss_rod:**
- 26: em_gss_phg:**
- 27: em_gss_vrl:**
- 28: gb_gss1:**
- 29: gb_gss2:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	311	96.3	343	12	B1319160	B1319160 949026D10
2	311	96.3	466	12	B1273504	B1273504 949026D10
3	311	96.3	471	12	B1245249	B1245249 949026D10
4	311	96.3	489	10	BG549370	BG549370 947074H12

5	311	96.3	566	12	B1478737	B1478737 949068G08
6	311	96.3	578	12	B1396085	B1396085 949044B04
7	311	96.3	580	12	B1674933	B1674933 949076E10
C 8	311	96.3	588	12	BG842079	BG842079 MEST35-H0
C 9	311	96.3	589	12	B1319097	B1319097 949039C04
10	311	96.3	619	12	B1430981	B1430981 949063F09
11	311	96.3	622	10	BG458523	BG458523 947045B08
12	311	96.3	652	9	AA979879	AA979879 MEST3-G2
13	310	96.0	817	9	AA979879	AA979879 MEST3-G2
C 14	309.4	95.8	475	12	B1319103	B1319103 949039D04
C 15	309.4	95.8	553	10	BE055905	BE055905 945017B11
C 16	309.4	95.8	629	9	AA979879	AA979879 MEST3-G2
17	307.8	95.3	1172	11	AY103730	AY103730 Zea mays
C 18	307.4	95.2	831	10	BG319747	BG319747 Zm03_05H0
C 19	307	95.0	574	10	BG517358	BG517358 947061E01
C 20	306.2	94.8	915	12	BG837761	BG837761 Zm10_05H0
C 21	306	94.7	495	12	B1643447	B1643447 949076E10
C 22	304.6	94.3	665	12	BM266503	BM266503 MEST382-B
C 23	299	92.6	694	9	AA979929	AA979929 MEST3-G11
C 24	295.2	91.4	704	10	BG320087	BG320087 Zm03_01Q0
C 25	293	90.7	660	10	BG320791	BG320791 Zm04_10C0
C 26	292.6	90.6	805	10	BG319818	BG319818 Zm03_08F1
C 27	289	89.5	513	12	B1431142	B1431142 949059C09
28	287	88.9	471	10	BG550428	BG550428 947074H12
29	287	88.9	521	12	B1595975	B1595975 949075C03
C 30	278	86.1	544	10	BG349334	BG349334 947028A12
C 31	276.2	85.5	673	12	BM078545	BM078545 MEST121-B
C 32	272.6	84.4	489	10	BG458372	BG458372 947044G04
C 33	271	83.9	638	12	B1993279	B1993279 1020075F0
C 34	271	83.9	655	12	BG842727	BG842727 MEST39-D0
C 35	271	83.9	732	12	BM080707	BM080707 MEST112-C
C 36	271	83.9	745	12	BG842572	BG842572 MEST33-E0
C 37	269.4	83.4	493	10	BE924836	BE924836 947011G10
C 38	268.8	83.2	550	12	B1674604	B1674604 949022F06
C 39	268.6	83.2	565	12	B1644173	B1644173 949022F06
40	267.2	82.7	445	12	B1675118	B1675118 949077G05
C 41	265.6	82.2	558	12	B1643515	B1643515 949077G05
C 42	265.6	82.2	570	12	B1675117	B1675117 949077G05
C 43	265	82.0	482	10	BG458792	BG458792 947054D04
C 44	262.6	81.3	705	10	BG320451	BG320451 Zm03_10F0
C 45	256	79.3	546	12	B1478736	B1478736 949068G08

ALIGNMENTS

RESULT 1	B1319160	B1319160	343 bp	mRNA	linear	EST 23-JUL-2001
LOCUS	949026D10.y1	949	-	Juvenile leaf and shoot	cDNA from Steve Moose	
DEFINITION	Zea mays	CDNA	mRNA	sequence.		
ACCESSION	B1319160	1	GI:14997085			
VERSION	B1319160.1					
KEYWORDS	EST.					
SOURCE	Zea mays					
ORGANISM	Zea mays					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.					
AUTHORS	Walbot V.					
TITLE	1 (bases 1 to 343)					
JOURNAL	Maize ESTs from various cDNA libraries sequenced at Stanford					
COMMENT	Unpublished					

Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 949026 row: D column: 10.
Location/Qualifiers


```
KEYWORDS EST.
SOURCE Zea mays
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
1. .471
  Location/Qualifiers
    /organism="Zea mays"
    /mol_type="mRNA"
    /cultivar="W64A"
    /db_xref="taxon:4577"
    /tissue_type="immature leaf primordium and vegetative meristem"
    /dev_stage="4 stages from 3-13 days after imbibing"
    /lab_host="E. coli XL0LR"
    /clone_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose"
    /note="Organ: juvenile vegetative shoots; Vector: pAD-GAL4-2.1; Site 1: EcoRI; Site 2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."
BASE COUNT 88 a 133 c 164 g 86 t
ORIGIN

Query Match 96.3%; Score 311; DB 12; Length 471;
Best Local Similarity 99.7%; Pred. No. 2.8e-61;
Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CGACCTGCTGAAGCAGGTGAGTACCTGCTGCGCAACGGCTGGATACCTGCTCGAGTT 60
DB 426 CGACCTGCTGAAGCAGGTGAGTACCTGCTGCGCAACGGCTGGATACCTGCTCGAGTT 367

QY 61 CAGCAAGGTGCGGCTTCGTGTACCGCGAGAACTCCACCTCCCGTGTCTACTACGACGGCG 120
DB 366 CAGCAAGGTGCGGCTTCGTGTACCGCGAGAACTCCACCTCCCGTGTCTACTACGACGGCG 307

QY 121 CTACTGGACCATGTGGAAGCATGCCCATGTTCGGCTGCAACGACGCCACCCAGGTGTACA 180
DB 306 CTACTGGACCATGTGGAAGC-TGCCCATGTTCGGCTGCAACGACGCCACCCAGGTGTACA 248

QY 181 AGAGCTGAGAGGGCCATCAATCTTACCGGACGCTTCCACCGCTCATCGGCTTCG 240
DB 247 AGAGCTGAGAGGGCCATCAATCTTACCGGACGCTTCCACCGCTCATCGGCTTCG 188

QY 241 ACAACATCAAGCAGCGAGTGGTTCAGCTTCATCGCTTACAGCCCCCGGCGAGGACT 300
DB 187 ACAACATCAAGCAGCGAGTGGTTCAGCTTCATCGCTTACAGCCCCCGGCGAGGACT 128

QY 301 AGACCGCGCGCGCGCGCGCC 323
```

```
Db 127 AGACCGCGCGCGCGCGCGCC 105

RESULT 4
BG549370
LOCUS
DEFINITION
  BG549370 489 bp mRNA linear EST 05-APR-2001
  947074H12.y1 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA
  sequence.
ACCESSION
  BG549370
VERSION
  BG549370.1 GI:13558014
KEYWORDS
  EST.
SOURCE
  Zea mays
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
    clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
  1 (bases 1 to 489)
AUTHORS
  Walbot V.
TITLE
  Maize ESTs from various cDNA libraries sequenced at Stanford
  University
JOURNAL
  Unpublished
COMMENT
  Contact: Walbot V
  Department of Biological Sciences
  Stanford University
  855 California Ave, Palo Alto, CA 94304, USA
  Tel: 650 723 2227
  Fax: 650 725 8221
  Email: walbot@stanford.edu
  Plate: 947074 row: H column: 12.
FEATURES
source
  1. .489
    Location/Qualifiers
      /organism="Zea mays"
      /mol_type="mRNA"
      /cultivar="B73"
      /db_xref="taxon:4577"
      /tissue_type="leaf and stem, including leaf base"
      /dev_stage="2 week old seedling (3 leaves)"
      /lab_host="XL1-Blue"
      /clone_lib="947 - 2 week shoot from Barkan lab"
      /note="Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-);
      Site 1: EcoRI; Site 2: XhoI; Directionally cloned using
      Stratagene's UniZap XR cDNA cloning kit with the 5' end
      at the EcoRI site. The library represents 8 x 10e5
      independent recombinant phage. The plants were greenhouse
      grown."
BASE COUNT 92 a 179 c 135 g 83 t
ORIGIN

Query Match 96.3%; Score 311; DB 10; Length 489;
Best Local Similarity 99.7%; Pred. No. 2.9e-61;
Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CGACCTGCTGAAGCAGGTGAGTACCTGCTGCGCAACGGCTGGATACCTGCTCGAGTT 60
DB 136 CGACCTGCTGAAGCAGGTGAGTACCTGCTGCGCAACGGCTGGATACCTGCTCGAGTT 195

QY 61 CAGCAAGGTGCGGCTTCGTGTACCGCGAGAACTCCACCTCCCGTGTCTACTACGACGGCG 120
DB 196 CAGCAAGGTGCGGCTTCGTGTACCGCGAGAACTCCACCTCCCGTGTCTACTACGACGGCG 255

QY 121 CTACTGGACCATGTGGAAGCATGCCCATGTTCGGCTGCAACGACGCCACCCAGGTGTACA 180
DB 256 CTACTGGACCATGTGGAAGC-TGCCCATGTTCGGCTGCAACGACGCCACCCAGGTGTACA 314

QY 181 AGAGCTGAGAGGGCCATCAATCTTACCGGACGCTTCCACCGCTCATCGGCTTCG 240
DB 315 AGAGCTGAGAGGGCCATCAATCTTACCGGACGCTTCCACCGCTCATCGGCTTCG 374

QY 241 ACAACATCAAGCAGCGAGTGGTTCAGCTTCATCGCTTACAGCCCCCGGCGAGGACT 300
DB 375 ACAACATCAAGCAGCGAGTGGTTCAGCTTCATCGCTTACAGCCCCCGGCGAGGACT 434

QY 301 AGACCGCGCGCGCGCGCGCC 323
```

Db	435	AGACCGCGCCGCCGCGCCCCC	457
RESULT 5			
BI478737			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Zea mays			
Zea mays			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD			
clade; Panicoideae; Andropogoneae; Zea.			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
CONTACT: Walbot V			
Department of Biological Sciences			
Stanford University			
855 California Ave, Palo Alto, CA 94304, USA			
Tel: 650 723 2227			
Fax: 650 725 8221			
Email: walbot@stanford.edu			
Plate: 949068 row: G column: 08.			
LOCATION/Qualifiers			
1..566			
/organism="Zea mays"			
/mol_type="mRNA"			
/db_xref="taxon:4577"			
/tissue_type="immature leaf primordium and vegetative meristem"			
/dev_stages="4 stages from 3-13 days after imbibing"			
/lab_host="E. coli XLOLR"			
/clone_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose"			
/note="Organ: juvenile vegetative shoots; Vector: pAD-GAL4-2.1; Site 1: EcoRI; Site 2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."			
BASE COUNT	107 a	205 c	162 g
ORIGIN			
Query Match			
Best Local Similarity	96.3%;	Score 311;	DB 12; Length 566;
Matches 322;	Conservative	0;	Mismatches 1; Gaps 1;
QY	1	CGACCTGCTGAACGAGGTGGACTTCTCTGCAGAACGGCTGGATACCCCTCGAGTT	60
Db	200	CGACCTGCTGAACGAGGTGGACTTCTCTGCAGAACGGCTGGATACCCCTCGAGTT	259
QY	61	CAGCAAGGTTCGGTTCGTGTACCGGAGAAGTCCACCTCTCCCGTGCTACTACGACGCCG	120
Db	260	CAGCAAGGTTCGGTTCGTGTACCGGAGAAGTCCACCTCTCCCGTGCTACTACGACGCCG	319
QY	121	CTATCGGACCATGTGAAGCATGCCCATTGTTTCGGCTGCAACGACGCCACCCAGGTGACA	180
b	320	CTATCGGACCATGTGAAGCATGCCCATTGTTTCGGCTGCAACGACGCCACCCAGGTGACA	378

```
Db 191 CGACCTGCTGAAGCAGGTGACTTACCTGCTGGCAACGGCTGGATACCTCGCTCGAGTT 250
    |||
QY 61 CAGCAAGGTGCGCTTCGCTGACCGGAGAACTCCACTCCCGTGTCTACTACGAGCGCG 120
    |||
Db 251 CAGCAAGGTGCGCTTCGCTGACCGGAGAACTCCACTCCCGTGTCTACTACGAGCGCG 310
    |||
QY 121 CTACTGGACCATGTGGAAGCATGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 180
    |||
Db 311 CTACTGGACCATGTGGAAGC-TGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 369
    |||
QY 181 AGGAGCTGCAGGAGGCCATCAATCTTACCGGAGCGCTTCCACCGGTCATCGGTTTCG 240
    |||
Db 370 AGGAGCTGCAGGAGGCCATCAATCTTACCGGAGCGCTTCCACCGGTCATCGGTTTCG 429
    |||
QY 241 ACAACATCAAGCAGACGCGTGGCTCAGCTTTCATCGCTTACAGCGCCCGGCGAGCGACT 300
    |||
Db 430 ACAACATCAAGCAGACGCGTGGCTCAGCTTTCATCGCTTACAGCGCCCGGCGAGCGACT 489
    |||
QY 301 AGACCGCGCCCGCGCGCCGCC 323
    |||
Db 490 AGACCGCGCCCGCGCGCCGCC 512
    |||

RESULT 7
B1674933
LOCUS
DEFINITION Zea mays cDNA, mRNA sequence.
ACCESSION B1674933
VERSION B1674933.1 GI:15590317
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 580)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 949076 row: E column: 10.
/dev_stage="4 stages from 3-13 days after imbibing"
/lab_host="E. coli XL0LR"
/clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
Moose"
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W64A"
/db_xref="taxon:4577"
/tissue_type="immature leaf primordium and vegetative
meristem"
/dev_stage="4 stages from 3-13 days after imbibing"
/lab_host="E. coli XL0LR"
/clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
Moose"
/note="Organ: juvenile vegetative shoots; Vector:
pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts
of total RNA by weight from 4 tissue sources (see below)
were pooled, polyA+ RNA isolated, and cDNA synthesized for
EcoRI (5') and XhoI (3') directional cloning into lambda
Hybridzap vector from Stratagene. Tissue Sources: 1. Whole
shoots 3 days after sowing/imbibing in wet soil. 2. Basal
1.5 cm shoots 6 days after sowing - includes yellow
portions of developing leaves 1-5, primordia from 6-8, and
the vegetative apex. 3. Non-green portions of developing
leaves 4-5 and the vegetative apex, including adult leaf
```

```
primordia, 9 days after sowing. 4. Partially expanded and
greening leaves 4-5 at 13 days after sowing."
BASE COUNT 108 a 215 c 168 g 89 t
ORIGIN
Query Match 96.3%; Score 311; DB 12; Length 580;
Best Local Similarity 99.7%; Pred. No. 3e-61;
Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 CGACCTGCTGAAGCAGGTGACTTACCTGCTGGCAACGGCTGGATACCTCGCTCGAGTT 60
    |||
Db 226 CGACCTGCTGAAGCAGGTGACTTACCTGCTGGCAACGGCTGGATACCTCGCTCGAGTT 285
    |||
QY 61 CAGCAAGGTGCGCTTCGCTGACCGGAGAACTCCACTCCCGTGTCTACTACGAGCGCG 120
    |||
Db 286 CAGCAAGGTGCGCTTCGCTGACCGGAGAACTCCACTCCCGTGTCTACTACGAGCGCG 345
    |||
QY 121 CTACTGGACCATGTGGAAGCATGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 180
    |||
Db 346 CTACTGGACCATGTGGAAGC-TGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 404
    |||
QY 181 AGGAGCTGCAGGAGGCCATCAATCTTACCGGAGCGCTTCCACCGGTCATCGGTTTCG 240
    |||
Db 405 AGGAGCTGCAGGAGGCCATCAATCTTACCGGAGCGCTTCCACCGGTCATCGGTTTCG 464
    |||
QY 241 ACAACATCAAGCAGACGCGTGGCTCAGCTTTCATCGCTTACAGCGCCCGGCGAGCGACT 300
    |||
Db 465 ACAACATCAAGCAGACGCGTGGCTCAGCTTTCATCGCTTACAGCGCCCGGCGAGCGACT 524
    |||
QY 301 AGACCGCGCCCGCGCGCCGCC 323
    |||
Db 525 AGACCGCGCCCGCGCGCCGCC 547
    |||

RESULT 8
B1674933
LOCUS
DEFINITION Zea mays cDNA, mRNA sequence.
ACCESSION B1674933
VERSION B1674933.1 GI:15590317
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 580)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
FCR Primers
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG) .
Location/Qualifiers
1..588
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="WEST35-H09"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
/clone_lib="ISUM3-TL"
/note="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI;
```

ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5' AACTGGAAGATTTCGCGCCGAGGAATTTTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT73PAC vector."

BASE COUNT	149 a	143 c	188 g	108 t
ORIGIN				
Query Match	96.3%; Score 311; DB 12; Length 588;			
Best Local Similarity	99.7%; Pred. No. 3e-61;			
Matches 322; Conservative	0; Mismatches 0; Indels 1; Gaps 1;			
QY	1 CGACCTGCTGAAGCAGGTGGACTACCTGCTGCGGAGAACTCCACCTCCCGTGTACTACGACGGCGG 120			
DB	577 CGACCTGCTGAAGCAGGTGGACTACCTGCTGCGGAGAACTCCACCTCCCGTGTACTACGACGGCGG 518			
QY	61 CAGCAAGGTGGCTTGGTGTACCGGAGAACTCCACCTCCCGTGTACTACGACGGCGG 120			
DB	517 CAGCAAGGTGGCTTGGTGTACCGGAGAACTCCACCTCCCGTGTACTACGACGGCGG 458			
QY	121 CTACTGGACATGTGAAGCATGCCATGTTGGCTGGAACGACGCGCCACCCAGGTGTACA 180			
DB	457 CTACTGGACATGTGAAGC-TGCCCATGTTGGCTGGAACGACGCGCCACCCAGGTGTACA 399			
QY	181 AGGAGCTGCAGGAGGCGCATCAATCTACCGGAGCGCTTCCACCGCGTCATCGGCTTCG 240			
DB	398 AGGAGCTGCAGGAGGCGCATCAATCTACCGGAGCGCTTCCACCGCGTCATCGGCTTCG 339			
QY	241 ACAACATCAAGCAGACGCGTGGTGTGAGTTTCATCGCTTACAGCCCGCGGCGGCGGACT 300			
DB	338 ACAACATCAAGCAGACGCGTGGTGTGAGTTTCATCGCTTACAGCCCGCGGCGGCGGACT 279			
QY	301 AGACCGCGCGCGCGCGCGCGCC 323			
DB	278 AGACCGCGCGCGCGCGCGCGCC 256			

RESULT 9
BI319097/c
LOCUS 949039C04.x2 949 - Juvenile leaf and shoot cDNA from Steve Moose
DEFINITION Zea mays cDNA, mRNA sequence.
ACCESSION BI319097
VERSION BI319097.1 GI:14996976
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 589)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL University
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 949039 row: C column: 04.
FEATURES
source Location/Qualifiers
1..589
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W64A"

/db xref="taxon:4577"
/tissue type="immature leaf primordium and vegetative meristem"
/dev stage="4 stages from 3-13 days after imbibing"
/lab_host="E. coli XL0LR"
/clone lib="949 - Juvenile leaf and shoot cDNA from Steve Moose"
/notes="Organ: juvenile vegetative shoots; Vector: PAD-GAL4-2.1; Site 1: EcoRI; Site 2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."

BASE COUNT	141 a	155 c	197 g	96 t
ORIGIN				
Query Match	96.3%; Score 311; DB 12; Length 589;			
Best Local Similarity	99.7%; Pred. No. 3e-61;			
Matches 322; Conservative	0; Mismatches 0; Indels 1; Gaps 1;			
QY	1 CGACCTGCTGAAGCAGGTGGACTACCTGCTGCGGAGAACTCCACCTCCCGTGTACTACGACGGCGG 60			
DB	502 CGACCTGCTGAAGCAGGTGGACTACCTGCTGCGGAGAACTCCACCTCCCGTGTACTACGACGGCGG 443			
QY	61 CAGCAAGGTGGCTTGGTGTACCGGAGAACTCCACCTCCCGTGTACTACGACGGCGG 120			
DB	442 CAGCAAGGTGGCTTGGTGTACCGGAGAACTCCACCTCCCGTGTACTACGACGGCGG 383			
QY	121 CTACTGGACATGTGAAGCATGCCATGTTGGCTGGAACGACGCGCCACCCAGGTGTACA 180			
DB	382 CTACTGGACATGTGAAGC-TGCCCATGTTGGCTGGAACGACGCGCCACCCAGGTGTACA 324			
QY	181 AGGAGCTGCAGGAGGCGCATCAATCTACCGGAGCGCTTCCACCGCGTCATCGGCTTCG 240			
DB	323 AGGAGCTGCAGGAGGCGCATCAATCTACCGGAGCGCTTCCACCGCGTCATCGGCTTCG 264			
QY	241 ACAACATCAAGCAGACGCGTGGTGTGAGTTTCATCGCTTACAGCCCGCGGCGGCGGACT 300			
DB	263 ACAACATCAAGCAGACGCGTGGTGTGAGTTTCATCGCTTACAGCCCGCGGCGGCGGACT 204			
QY	301 AGACCGCGCGCGCGCGCGCGCC 323			
DB	203 AGACCGCGCGCGCGCGCGCGCC 181			

RESULT 10
BI430981
LOCUS 949063P09.y1 949 - Juvenile leaf and shoot cDNA from Steve Moose
DEFINITION Zea mays cDNA, mRNA sequence.
ACCESSION BI430981
VERSION BI430981.1 GI:15209097
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 619)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL University
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University

855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 949063 row: F column: 09.

FEATURES source

Location/Qualifiers
1. .619
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W64A"
/db_xref="taxon:4577"
/tissue_type="immature leaf primordium and vegetative meristem"
/dev_stage="4 stages from 3-13 days after imbibing"
/lab_host="E. coli XL0LR"
/clone_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose"

/note="Organ: juvenile vegetative shoots; Vector: pAD-GAL4-2.1; Site_1: EcoRI; Site_2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia. 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."

BASE COUNT 110 a 225 c 177 g 107 t
ORIGIN

Query Match 96.3%; Score 311; DB 12; Length 619;

Best Local Similarity 99.7%; Pred. No. 3e-61; Indels 1; Gaps 1; Matches 322; Conservative 0; Mismatches 0;

QY 1 CGACCTGCTGAAGCAGGTGGACTACTCTGCTGGCGCAACGGCTGGATACCCCTGCTCGAGTT 60
Db 208 CGACCTGCTGAAGCAGGTGGACTACTCTGCTGGCGCAACGGCTGGATACCCCTGCTCGAGTT 267

QY 61 CAGCAAGTTCGCTTCGTGTACCGGAGAACTCCACCTCCCGTGTACTACGACGGCG 120
Db 268 CAGCAAGTTCGCTTCGTGTACCGGAGAACTCCACCTCCCGTGTACTACGACGGCG 327

QY 121 CTACTGGACCATGTGGAAGC- TGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 180
Db 328 CTACTGGACCATGTGGAAGC- TGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 386

QY 181 AGGAGCTGCAGGAGCCATCAATCTACCGGAGCGCTTCCACCGCGTCATCGGCTTCG 240
Db 387 AGGAGCTGCAGGAGCCATCAATCTACCGGAGCGCTTCCACCGCGTCATCGGCTTCG 446

QY 241 ACAACATCAAGCAGACGAGTGGTTCATCGCTTACAGCCCGCGGACGAGT 300
Db 447 ACAACATCAAGCAGACGAGTGGTTCATCGCTTACAGCCCGCGGACGAGT 506

QY 301 AGACCGCGCCCGCGGCGCCCC 323
Db 507 AGACCGCGCCCGCGGCGCCCC 529

RESULT 11

LOCUS BG458523 622 bp mRNA linear EST 19-MAR-2001
DEFINITION 947045808.y1 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA sequence.

ACCESSION BG458523
VERSION BG458523.1 GI:13381848

KEYWORDS EST.
SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 622)

Walbot V.

Maize ESTs from various cDNA libraries sequenced at Stanford University

Unpublished

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave., Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 947045 row: B column: 08.

FEATURES source

1. 622
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"

/db_xref="taxon:4577"

/tissue_type="leaf and stem, including leaf base"

/dev_stage="2 week old seedling (3 leaves)"

/lab_host="XLI-Blue"

/clone_lib="947 - 2 week shoot from Barkan lab"

/note="Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-); Site 1: EcoRI; Site 2: XhoI; Directionally cloned using Stratagene's UniZap_XR cDNA cloning kit with the 5' end at the EcoRI site. The library represents 8 x 10⁵ independent recombinant phage. The plants were greenhouse grown."

BASE COUNT 117 a 224 c 172 g 109 t
ORIGIN

Query Match 96.3%; Score 311; DB 10; Length 622;

Best Local Similarity 99.7%; Pred. No. 3e-61; Indels 1; Gaps 1; Matches 322; Conservative 0; Mismatches 0;

QY 1 CGACCTGCTGAAGCAGGTGGACTACTCTGCTGGCGCAACGGCTGGATACCCCTGCTCGAGTT 60
Db 244 CGACCTGCTGAAGCAGGTGGACTACTCTGCTGGCGCAACGGCTGGATACCCCTGCTCGAGTT 303

QY 61 CAGCAAGTTCGCTTCGTGTACCGGAGAACTCCACCTCCCGTGTACTACGACGGCG 120
Db 304 CAGCAAGTTCGCTTCGTGTACCGGAGAACTCCACCTCCCGTGTACTACGACGGCG 363

QY 121 CTACTGGACCATGTGGAAGCATGCCCATGTTCCGCTGCAACGACGCCACCCAGGTGTACA 180
Db 364 CTACTGGACCATGTGGAAGC- TGCCCATGTTGGCTGCAACGACGCCACCCAGGTGTACA 422

QY 181 AGGAGCTGCAGGAGCCATCAATCTACCGGAGCGCTTCCACCGCGTCATCGGCTTCG 240
Db 423 AGGAGCTGCAGGAGCCATCAATCTACCGGAGCGCTTCCACCGCGTCATCGGCTTCG 482

QY 241 ACAACATCAAGCAGACGAGTGGTTCATCGCTTACAGCCCGCGGACGAGT 300
Db 483 ACAACATCAAGCAGACGAGTGGTTCATCGCTTACAGCCCGCGGACGAGT 542

QY 301 AGACCGCGCCCGCGGCGCCCC 323
Db 543 AGACCGCGCCCGCGGCGCCCC 565

RESULT 12

LOCUS AW352495

DEFINITION 707050B11.y1 707 - Mixed adult tissues from Walbot lab (SK) Zea mays cDNA, mRNA sequence.

ACCESSION AW352495

VERSION AW352495.1 GI:6851485

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE AUTHORS TITLE JOURNAL COMMENT	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	
	1 (bases 1 to 652)		1 (bases 1 to 817)	
	Walbot.V.		Wen,T.J., Ashlock,D.A. and Schnable,P.S.	
	Maize ESTs from various cDNA libraries sequenced at Stanford University		Expressed Sequence Tags from B73 Maize Seedlings	
	Unpublished		Unpublished	
FEATURES source	Contact: Walbot V		Contact: Schnable, PS	
	Department of Biological Sciences		Schnable Laboratory	
	Stanford University		Iowa State University	
	855 California Ave, Palo Alto, CA 94304, USA		G405 Agronomy, Ames, IA 50011, USA	
	Tel: 650 723 2227		Tel: (515)-294-0975	
FEATURES source	Fax: 650 725 8221		Fax: (515)-294-2299	
	Email: walbot@stanford.edu		Email: schnable@iastate.edu	
	Plate: 707050 row: B column: 11.		PCR Primers	
	Location/Qualifiers		FORWARD: tw1412 (5'-GAAGATACCCCAACACC-3')	
	1..652		BACKWARD: T7-YJ (5'-TAATACGACTCATATAGGC-3')	
FEATURES source	/organism="Zea mays"		/organism="Zea mays"	
	/mol_type="mRNA"		/mol_type="mRNA"	
	/cultivar="W23"		/cultivar="B73"	
	/db_xref="taxon:4577"		/db_xref="taxon:4577"	
	/tissue_type="tassel, kernel, silk, husk, root, leaf"		/tissue_type="above ground tissues"	
BASE COUNT ORIGIN	/dev_stage="adult"		/dev_stage="Two-leaf-stage green seedling"	
	/lab_host="DH10B"		/lab_host="XLI-MFR Blue"	
	/clone_lib="707 - Mixed adult tissues from Walbot lab (SK)"		/clone_lib="ISUM2"	
	130 a 237 c 185 g 100 t		/notes="Organ: green seedlings; Vector: PAD-GAL4; Site_1: EcoRI; Site 2: XhoI; ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer. The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Pol-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the HybriZAP lambda vector (Stratagene) and excised as PAD-GAL4 phagemids."	
	Query Match 96.3%; Score 311; DB 9; Length 652;		BASE COUNT 149 a 267 c 213 g 178 t 10 others	
QY	Best Local Similarity 99.7%; Pred. No. 3e-61; Indels 1; Gaps 1;		ORIGIN	
	Matches 322; Conservative 0; Mismatches 0; Indels 1; Gaps 1;		Query Match 96.0%; Score 310; DB 9; Length 817;	
	1 CGACCTGCTGAAGCAGGTGACTACCTGCTGCGCAACGGCTGATACCTGCTCGAGTT 60		Best Local Similarity 99.4%; Pred. No. 5.4e-61;	
	286 CGACCTGCTGAAGCAGGTGACTACCTGCTGCGCAACGGCTGATACCTGCTCGAGTT 345		Matches 321; Conservative 0; Mismatches 1; Indels 1; Gaps 1;	
	61 CAGCAAGGTGGCTTGGTACCGCGAGAACTCCACTCCCGTGTACTACGACGGCG 120		QY 1 CGACCTGCTGAAGCAGGTGACTACCTGCTGCGCAACGGCTGATACCTGCTCGAGTT 60	
QY	346 CAGCAAGGTGGCTTGGTACCGCGAGAACTCCACTCCCGTGTACTACGACGGCG 405		Db 252 CGACCTGCTGAAGCAGGTGACTACCTGCTGCGCAACGGCTGATACCTGCTCGAGTT 311	
	121 CTACTGGACCATGTGGAGCATGCCATGTTCCGGCTGCAACGACGCCACCCAGGTGTACA 180		QY 61 CAGCAAGGTGGCTTGGTACCGCGAGAACTCCACTCCCGTGTACTACGACGGCG 120	
	406 CTACTGGACCATGTGGAGC-TGCCCATGTTCCGGCTGCAACGACGCCACCCAGGTGTACA 464		Db 312 CAGCAAGGTGGCTTGGTACCGCGAGAACTCCACTCCCGTGTACTACGACGGCG 371	
	181 AGGAGCTGCAGGAGGCGCATCAATCTCTACCGGACGCTTCCACCGGTTCG 240		QY 121 CTACTGGACCATGTGGAGCATGCCATGTTCCGGCTGCAACGACGCCACCCAGGTGTACA 180	
	465 AGGAGCTGCAGGAGGCGCATCAATCTCTACCGGACGCTTCCACCGGTTCG 524		Db 372 CTACTGGACCATGTGGAGC-TGCCCATGTTCCGGCTGCAACGACGCCACCCAGGTGTACA 430	
QY	241 ACAACATCAAGCAGACGAGTGGTTCATCGCTTACAGCCCCCGGGCAGCGACT 300		QY 181 AGGAGCTGCAGGAGGCGCATCAATCTCTACCGGACGCTTCCACCGGTTCG 240	
	525 ACAACATCAAGCAGACGAGTGGTTCATCGCTTACAGCCCCCGGGCAGCGACT 584		Db 431 AGGAGCTGCAGGAGGCGCATCAATCTCTACCGGACGCTTCCACCGGTTCG 490	
	301 AGACCGCGCCCGCGCGCGCCCC 323		QY 241 ACAACATCAAGCAGACGAGTGGTTCATCGCTTACAGCCCCCGGGCAGCGACT 300	
	585 AGACCGCGCCCGCGCGCGCCCC 607		Db 491 ACAACATCAAGCAGACGAGTGGTTCATCGCTTACAGCCCCCGGGCAGCGACT 550	
	RESULT 13		QY 301 AGACCGCGCCCGCGCGCGCCCC 323	
LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	AA979879		Db 551 AGACCGCGCCCGCGCGCGCCCC 573	
	AA979879		RESULT 13	
	MEST2-G2.Tw1412.Seq ISUM2 Zea mays cDNA clone MEST2-G2 5', mRNA		AA979879	
	sequence.		LOCUS	
	AA979879.1 GI:3157257		DEFINITION	

```

RESULT 14
BI319103/c
LOCUS
DEFINITION
  BI319103 475 bp mRNA linear EST 23-JUL-2001
  949039D04.x2 949 - Juvenile leaf and shoot cDNA from Steve Moose
  Zea mays cDNA, mRNA sequence.
ACCESSION
  BI319103
VERSION
  BI319103.1 GI:14996985
KEYWORDS
  EST.
SOURCE
  Zea mays
  Zea mays
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Zea.
  Walbot.V.
REFERENCE
  Zea ESTs from various cDNA libraries sequenced at Stanford
AUTHORS
  University
TITLE
  Unpublished
JOURNAL
  Contact: Walbot V
COMMENT
  Department of Biological Sciences
  Stanford University
  855 California Ave, Palo Alto, CA 94304, USA
  Tel: 650 723 2227
  Fax: 650 725 8221
  Email: walbot@stanford.edu
  Plate: 949039 row: D column: 04.
  Location/Qualifiers
  1..475
  /organism="Zea mays"
  /mol_type="mRNA"
  /cultivar="W64A"
  /db_xref="taxon:4577"
  /tissue_type="immature leaf primordium and vegetative
  meristem"
  /dev_stage="4 stages from 3-13 days after imbibing"
  /lab_host="E. coli XL0LR"
  /clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
  Moose"
  /note="Organ: juvenile vegetative shoots; Vector:
  pAD-GAL4-2.1; Site:1: EcoRI; Site:2: XhoI; Equal amounts
  of total RNA by weight from 4 tissue sources (see below)
  were pooled, polyA+ RNA isolated, and cDNA synthesized for
  EcoRI (5') and XhoI (3') directional cloning into lambda
  Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
  shoots 3 days after sowing/imbibing in wet soil. 2. Basal
  1.5 cm shoots 6 days after sowing - includes yellow
  portions of developing leaves 1-5, primordia from 6-8, and
  the vegetative apex. 3. Non-green portions of developing
  leaves 4-5 and the vegetative apex, including adult leaf
  primordia, 9 days after sowing. 4. Partially expanded and
  greening leaves 4-5 at 13 days after sowing."
  110 a 123 c 164 g 78 t
  BASE COUNT
  ORIGIN
  Query Match 95.8%; Score 309.4; DB 12; Length 475;
  Best Local Similarity 99.4%; Pred. No. 6.6e-61;
  Matches 321; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

  QY 1 CGACCTGTGAAGCAGGTGGACTACTGCTGCGCAACGCGTGGATACCTCGCTCGAGTT 60
  Db 475 CGACCTGTGAAGCAGGTGGACTACTGCTGCGCAACGCGTGGATACCTCGCTCGAGTT 416

  QY 61 CAGCAAGGTGCGCTTCGTGTACCGGAGACTCCACCTCCCGTGTACTACGACGGCG 120
  Db 415 CAGCAAGGTGCGCTTCGTGTACCGGAGAAACCCACCTCCCGTGTACTACGACGGCG 356

  QY 121 CTACTGGACCATGTGGAAGCATGCCATGTCGGCTGCAACGACGCCACCGAGGTGACA 180
  Db 355 CTACTGGACCATGTGGAAGC - TGCCCATGTTCCGGCTGCAACGACGCCACCGAGGTGACA 297

  QY 181 AGGAGCTGCAGGAGGCCATCAAAATCCTACCCCGAGCGCCTTCCACCGCGCTCATCGGCTTCG 240
  101 a 197 c 157 g 98 t
  BASE COUNT
  ORIGIN
  Query Match 95.8%; Score 309.4; DB 10; Length 553;
  Best Local Similarity 99.4%; Pred. No. 6.8e-61;
  Matches 321; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

  QY 1 CGACCTGTGAAGCAGGTGGACTACTGCTGCGCAACGCGTGGATACCTCGCTCGAGTT 60
  Db 138 CGATCTGTGAAGCAGGTGGACTACTGCTGCGCAACGCGTGGATACCTCGCTCGAGTT 197

  QY 61 CAGCAAGGTGCGCTTCGTGTACCGGAGAACTCCACCTCCCGTGTACTACGACGGCG 120
  Db 198 CAGCAAGGTGCGCTTCGTGTACCGGAGAACTCCACCTCCCGTGTACTACGACGGCG 257

  QY 121 CTACTGGACCATGTGGAAGCATGCCATGTCGGCTGCAACGACGCCACCGAGGTGACA 180
  Db 258 CTACTGGACCATGTGGAAGC - TGCCCATGTTCCGGCTGCAACGACGCCACCGAGGTGACA 316

```

